

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/517,645
Source: PCR
Date Processed by STIC: 1/26/06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 01/26/2006

PATENT APPLICATION: US/10/517,645

TIME: 08:52:28

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\01262006\J517645.raw

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4 <110> APPLICANT: Prigent, Claude
5   Martin, Anne
7 <120> TITLE OF INVENTION: Anti-Aurora-A Monoclonal Antibody,
8   Method For Obtaining Same, and Uses Thereof For Diagnosing
9   and Treating Cancers
11 <130> FILE REFERENCE: 50376/004001
13 <140> CURRENT APPLICATION NUMBER: US 10/517,645
14 <141> CURRENT FILING DATE: 2004-12-10
16 <150> PRIOR APPLICATION NUMBER: PCT/FR03/01772
17 <151> PRIOR FILING DATE: 2003-06-12
19 <150> PRIOR APPLICATION NUMBER: FR 02/07212
20 <151> PRIOR FILING DATE: 2002-06-12
22 <160> NUMBER OF SEQ ID NOS: 2
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 2253
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (257)...(1468)
35 <400> SEQUENCE: 1
36 ggaagacttg ggtccttggg tcgcaggtgg gagccgacgg gtgggtagac cgtgggggat 60
37 atctcagtg cggacgagga cggcggggac aaggggcggc tggtcggagt ggcggagcgt 120
38 caagtccctt gtcggttcc cgcctccctga gtgtccttgg cgctgccttg tgcccgccta 180
39 gcgcctttgc atccgctcct gggcaccgag gcgccttgta ggatactgct tgttacttat 240
40 tacagctaga ggcatac atg gac cga tct aaa gaa aac tgc att tca gga cct 292
41           Met Asp Arg Ser Lys Glu Asn Cys Ile Ser Gly Pro
42           1           5           10
44 gtt aag gct aca gct cca gtt gga ggt cca aaa cgt gtt ctc gtg act 340
45 Val Lys Ala Thr Ala Pro Val Gly Pro Lys Arg Val Leu Val Thr
46           15           20           25
48 cag caa att cct tgt cag aat cca tta cct gta aat agt ggc cag gct 388
49 Gln Gln Ile Pro Cys Gln Asn Pro Leu Pro Val Asn Ser Gly Gln Ala
50           30           35           40
52 cag cgg gtc ttg tgt cct tca aat tct tcc cag cgc gtt cct ttg caa 436
53 Gln Arg Val Leu Cys Pro Ser Asn Ser Ser Gln Arg Val Pro Leu Gln
54 45           50           55           60
56 gca caa aag ctt gtc tcc agt cac aag ccg gtt cag aat cag aag cag 484
57 Ala Gln Lys Leu Val Ser Ser His Lys Pro Val Gln Asn Gln Lys Gln
58           65           70           75
60 aag caa ttg cag gca acc agt gta cct cat cct gtc tcc agg cca ctg 532
61 Lys Gln Leu Gln Ala Thr Ser Val Pro His Pro Val Ser Arg Pro Leu

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62		80		85		90		
64	aat aac acc	caa aag agc aag	cag ccc ctg cca	tcg gca cct	gaa aat	580		
65	Asn Asn Thr	Gln Lys Ser Lys	Gln Pro Leu Pro	Ser Ala Pro	Glu Asn			
66		95		100		105		
68	aat cct gag	gag gaa ctg gca	tca aaa cag aaa	aat gaa tca	aaa	628		
69	Asn Pro Glu	Glu Glu Leu Ala	Ser Lys Gln Lys	Asn Glu Glu	Ser Lys			
70		110		115		120		
72	aag agg cag	tgg gct ttg gaa	gac ttt gaa att	ggg cgc cct	ctg ggt	676		
73	Lys Arg Gln	Trp Ala Leu Glu	Asp Phe Glu Ile	Gly Arg Pro	Leu Gly			
74	125		130		135		140	
76	aaa gga aag	ttt ggt aat gtt	tat ttg gca aga	gaa aag caa	agc aag	724		
77	Lys Gly Lys	Phe Gly Asn Val	Tyr Leu Ala Arg	Glu Lys Gln	Ser Lys			
78		145		150		155		
80	ttt att ctg	gct ctt aaa gtg	tta ttt aaa gct	cag ctg gag	aaa gcc	772		
81	Phe Ile Leu	Ala Leu Lys Val	Leu Phe Lys Ala	Gln Leu Glu	Lys Ala			
82		160		165		170		
84	gga gtg gag	cat cag ctc aga	aga gaa gta gaa	ata cag tcc	cac ctt	820		
85	Gly Val Glu	His Gln Leu Arg	Arg Glu Val Glu	Ile Gln Ser	His Leu			
86		175		180		185		
88	cgg cat cct	aat att ctt aga	ctg tat ggt tat	ttc cat gat	gct acc	868		
89	Arg His Pro	Asn Ile Leu Arg	Leu Tyr Gly Tyr	Phe His Asp	Ala Thr			
90		190		195		200		
92	aga gtc tac	cta att ctg gaa	tat gca cca ctt	gga aca gtt	tat aga	916		
93	Arg Val Tyr	Leu Ile Leu Glu	Tyr Ala Pro Leu	Gly Thr Val	Tyr Arg			
94	205		210		215		220	
96	gaa ctt cag	aaa ctt tca aag	ttt gat gag cag	aga act gct	act tat	964		
97	Glu Leu Gln	Lys Leu Ser Lys	Phe Asp Glu Gln	Arg Thr Ala	Thr Tyr			
98		225		230		235		
100	ata aca gaa	ttg gca aat gcc	ctg tct tac tgt	cat tcg aag	aga gtt	1012		
101	Ile Thr Glu	Leu Ala Asn Ala	Leu Ser Tyr Cys	His Ser Lys	Arg Val			
102		240		245		250		
104	att cat aga	gac att aag cca	gag aac tta ctt	ctt gga tca	gct gga	1060		
105	Ile His Arg	Asp Ile Lys Pro	Glu Asn Leu Leu	Leu Gly Ser	Ala Gly			
106		255		260		265		
108	gag ctt aaa	att gca gat ttt	ggg tgg tca gta	cat gct cca	tct tcc	1108		
109	Glu Leu Lys	Ile Ala Asp Phe	Gly Trp Ser Val	His Ala Pro	Ser Ser			
110		270		275		280		
112	agg agg acc	act ctc tgt ggc	acc ctg gac tac	ctg ccc cct	gaa atg	1156		
113	Arg Arg Thr	Thr Leu Cys Gly	Thr Leu Asp Tyr	Leu Pro Pro	Glu Met			
114	285		290		295		300	
116	att gaa ggt	cgg atg cat gat	gag aag gtg gat	ctc tgg agc	ctt gga	1204		
117	Ile Glu Gly	Arg Met His Asp	Glu Lys Val Asp	Leu Trp Ser	Leu Gly			
118		305		310		315		
120	gtt ctt tgc	tat gaa ttt tta	gtt ggg aag cct	cct ttt gag	gca aac	1252		
121	Val Leu Cys	Tyr Glu Phe Leu	Val Gly Lys Pro	Pro Phe Glu	Ala Asn			
122		320		325		330		
124	aca tac caa	gag acc tac aaa	aga ata tca cgg	gtt gaa ttc	aca ttc	1300		
125	Thr Tyr Gln	Glu Thr Tyr Lys	Arg Ile Ser Arg	Val Glu Phe	Thr Phe			
126		335		340		345		

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128 cct gac ttt gta aca gag gga gcc agg gac ctc att tca aga ctg ttg 1348
129 Pro Asp Phe Val Thr Glu Gly Ala Arg Asp Leu Ile Ser Arg Leu Leu
130 350 355 360
132 aag cat aat ccc agc cag agg cca atg ctc aga gaa gta ctt gaa cac 1396
133 Lys His Asn Pro Ser Gln Arg Pro Met Leu Arg Glu Val Leu Glu His
134 365 370 375 380
136 ccc tgg atc aca gca aat tca tca aaa cca tca aat tgc caa aac aaa 1444
137 Pro Trp Ile Thr Ala Asn Ser Ser Lys Pro Ser Asn Cys Gln Asn Lys
138 385 390 395
140 gaa tca gct agc aaa cag tct tag gaatcgtgca gggggagaaaa tccttgagcc 1498
141 Glu Ser Ala Ser Lys Gln Ser *
142 400
144 agggctgccataataacctga caggaacatg ctactgaagt ttattttacc attgactgct 1558
145 gccctcaatc tagaacgcta cacaagaaat atttgtttta ctcagcagggt gtgccttaac 1618
146 ctccctattc agaaagctcc acatcaataa acatgacact ctgaagtgaag agtagccacg 1678
147 agaattgtgc tacttatact gggttcataat ctggaggcaa gggttcgactg cagccgcccc 1738
148 gtcagcctgt gctagggcatg gtgtcttcac aggaggcaaa tccagagcct ggctgtgggg 1798
149 aaagtgaacca ctctgccctg accccgatca gttaaggagc tgtgcaataa ccttcctagt 1858
150 acctgagtga gtgtgtaact tattgggttg gcgaagcctg gtaaagctgt tggaatgagt 1918
151 atgtgattct ttttaagtat gaaaataaag atatatgtac agacttgat tttttctctg 1978
152 gtggcattcc ttttagaatg ctgtgtgtct gtccggcacc ccggtaggcc tgattgggtt 2038
153 tctagtctc cttaccact tatctccat atgagagtgt gaaaaatagg aacacgtgct 2098
154 ctacctccat ttagggattt gcttgggata cagaagaggc catgtgtctc agagctgtta 2158
155 agggcttatt tttttaaaac attggagtca tagcatgtgt gtaaaacttta aatatgcaaa 2218
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159 <211> LENGTH: 403
160 <212> TYPE: PRT
161 <213> ORGANISM: Homo sapiens
163 <400> SEQUENCE: 2
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165 1 5 10 15
166 Ala Pro Val Gly Gly Pro Lys Arg Val Leu Val Thr Gln Gln Ile Pro
167 20 25 30
168 Cys Gln Asn Pro Leu Pro Val Asn Ser Gly Gln Ala Gln Arg Val Leu
169 35 40 45
170 Cys Pro Ser Asn Ser Ser Gln Arg Val Pro Leu Gln Ala Gln Lys Leu
171 50 55 60
172 Val Ser Ser His Lys Pro Val Gln Asn Gln Lys Gln Lys Gln Leu Gln
173 65 70 75 80
174 Ala Thr Ser Val Pro His Pro Val Ser Arg Pro Leu Asn Asn Thr Gln
175 85 90 95
176 Lys Ser Lys Gln Pro Leu Pro Ser Ala Pro Glu Asn Asn Pro Glu Glu
177 100 105 110
178 Glu Leu Ala Ser Lys Gln Lys Asn Glu Glu Ser Lys Lys Arg Gln Trp
179 115 120 125
180 Ala Leu Glu Asp Phe Glu Ile Gly Arg Pro Leu Gly Lys Gly Lys Phe
181 130 135 140
182 Gly Asn Val Tyr Leu Ala Arg Glu Lys Gln Ser Lys Phe Ile Leu Ala

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183 145          150          155          160
184 Leu Lys Val Leu Phe Lys Ala Gln Leu Glu Lys Ala Gly Val Glu His
185          165          170          175
186 Gln Leu Arg Arg Glu Val Glu Ile Gln Ser His Leu Arg His Pro Asn
187          180          185          190
188 Ile Leu Arg Leu Tyr Gly Tyr Phe His Asp Ala Thr Arg Val Tyr Leu
189          195          200          205
190 Ile Leu Glu Tyr Ala Pro Leu Gly Thr Val Tyr Arg Glu Leu Gln Lys
191          210          215          220
192 Leu Ser Lys Phe Asp Glu Gln Arg Thr Ala Thr Tyr Ile Thr Glu Leu
193 225          230          235          240
194 Ala Asn Ala Leu Ser Tyr Cys His Ser Lys Arg Val Ile His Arg Asp
195          245          250          255
196 Ile Lys Pro Glu Asn Leu Leu Leu Gly Ser Ala Gly Glu Leu Lys Ile
197          260          265          270
198 Ala Asp Phe Gly Trp Ser Val His Ala Pro Ser Ser Arg Arg Thr Thr
199          275          280          285
200 Leu Cys Gly Thr Leu Asp Tyr Leu Pro Pro Glu Met Ile Glu Gly Arg
201          290          295          300
202 Met His Asp Glu Lys Val Asp Leu Trp Ser Leu Gly Val Leu Cys Tyr
203 305          310          315          320
204 Glu Phe Leu Val Gly Lys Pro Pro Phe Glu Ala Asn Thr Tyr Gln Glu
205          325          330          335
206 Thr Tyr Lys Arg Ile Ser Arg Val Glu Phe Thr Phe Pro Asp Phe Val
207          340          345          350
208 Thr Glu Gly Ala Arg Asp Leu Ile Ser Arg Leu Leu Lys His Asn Pro
209          355          360          365
210 Ser Gln Arg Pro Met Leu Arg Glu Val Leu Glu His Pro Trp Ile Thr
211          370          375          380
212 Ala Asn Ser Ser Lys Pro Ser Asn Cys Gln Asn Lys Glu Ser Ala Ser
213 385          390          395          400
214 Lys Gln Ser

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VERIFICATION SUMMARY

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